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## ALIGNMENTS

RESULT 1
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XX alkaline bovine; b Bos (HOFF EP1176205-A2 Bovine bIAPII ADI26549 30-JAN-2002. 22-APR-2004 25-JUL-2000; 21-JUL-2001; taurus. ROCHE DIAGNOSTICS GMBH.
HOFFMANN LA ROCHE & CO AG F. phosphatase; resistance gene; zeomycin; G418; bIAPII; yeast; gene; ds. standard; 2000DE-01036491. 2001EP-00117822. (first DNA. DNA; 1476 BP. applicant heat stability;

Mueller R, TI Kirschbaum T, Thalhofer J, lhofer J, Geipel Bommarius B; , H Hoelke W, Glaser ა ა Eckstein Ξ,

WPI; 2002-173 23/23

Preparing eukaryotic alkaline and for dephosphorylation, by for high gene copy number. phosphatase, recombinant expression diagnostic reagent in yeast selected

Claim 2; SEQ ID NO 1; 23pp; German.

This invention of phosphatase in gene sequence in purifying. A fin selection marked and alkaline phosphataline pho medium containing a marker In describes a novel method of preparing eukaryotic alkaline in yeast cells, comprising cloning an alkaline phosphatase into different vectors, transforming, and expressing and first vector is used containing a resistance gene against a ker and transformants that have integrated resistance gene phosphatase gene into the genome are selected by growth on ning a low concentration of selection marker. The gene copy

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selected on growth medium under high selection pressure. A second vector containing the alkaline phosphatase gene and a second resistance gene against a second marker is introduced, its copy number increased as for the first resistance gene and clones selected that have many copies of the alkaline phosphatase gene and of both resistance genes, integrated into the genome. The vectors used in the method are pHAP10-3 and pHAP10-3/9K. Preferred cells include methylotrophic yeast, particularly Pichia pastoris and Hansenula polymorpha and specifically P. pastoris X-33 cransformed with phAP10-3 and pHAP10-3/9K. The amino acid sequence of bovine alkaline phosphatase is known and, working back from this, an optimised codon sequence was designed. This was assembled conventionally from 28 synthetic oligonucleotides to give a sequence having EcoRI and Asp718 recognition sites at the ends to facilitate cloning. The selection markers are particularly zeomycin and G418, respectively. The alkaline phosphatase is used as diagnostic reagent, as part of a conjugate and for dephosphorylation of DNA. This method produces very active, glycosylated calkaline phosphatase with specific activity over 3000, preferably 10000, units/mg and heat stability comparable with that for commercial enzymes. The expression without any selection pressure. This sequence represents the covine bIAPII gene.
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Best Local Similarity

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Matches 1456; Conservative
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15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
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P-PSDB; AAM78362.
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P-PSDB; AAR91805.

Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprise AP fused downstream of antibody heavy or light chain, useful as immunoassay reagent.

Example 1; Page 10-12; 44pp; Japanese.

The gene coding for human alkaline phosphatase is fused downstream of a gene coding for either the variable and CH1 regions of an antibody heavy chain or an antibody light chain. Coexpression of the H- and L-chain sequences, one of which is fused to the AP gene, results in production of AP-labelled antibodies suitable for use in immunoassays. The present sequence codes for human AP

Sequence 1587 BP; 317 A; 515 C; 490 G; 265 T; 0 U; 0 Other;

Query Match 70.0%; Score 1032.6; DB 2; Length 1587; Best Local Similarity 81.4%; Pred. No. 4.5e-241; Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

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Obtaining vascular s selecting genes.
The present invention relates to a method for obtaining a vasodilating substance which increases expression of vasodilation response genes, and obtaining a vasodepressor which increases or decreases the expression level of vasodilation response genes. The method is useful for obtaining vasodilating substance which increases/decreases expression of vasodilation response genes. The vasodepressor substance obtained by the method of the invention is useful as an antihypertensive drug. The method is also useful for identifying the specific vasodilator-response genes. The present sequence represents a human vasodilator-responsive gene.
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ASAHI KASEI KK.
SUMITOMO SEIYAKU
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                                                                              The present invention describes a method for detecting high-grade dysplasia (HGD) in cells of a mammalian tissue sample. Also described: (1) identifying an oesophageal tissue susceptible to oesophageal adenocarcinoma; (2) determining the predisposition of a mammalian tissue to a neo-plastic transformation by detecting HGD in cells of the tissue; and (3) detecting cancer in a patient. The method can be used in detecting HGD and cancer in cells of a mammalian tissue sample. The methods and compositions of the present invention can be used in treating and preventing HGD and cancer, and in gene therapy. The present sequence encodes human alkaline phosphatase intestinal precursor (PPBI), which is used in the exemplification of the present invention. The human PPBI gene is located on chromosome 2.
                                                                                                                                                                                                                                                                                     Detecting of high-grade dysplasia in cells of a mammalian tissue sampl comprises establishing the level of expression in the test tissue samp of the genes.
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 Score 1032.6; DB 12;
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Chien D, Elliott VS,
Harmssen BW, Ho A, I;
Marquis JP, Murage J,
Swarnakar A, Tang TY,
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ng BM, Favero KD, Haf

Khare R, Lee S, Lee

n DB, Ramkumar J, Ric

TT, Yue H,
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(D, Hafalia AJA;
S, Lee SY, Lu DAM;
J, Richardson TW;
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New human secreted protein (SECP) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of functional SECP e.g., autoimmune disorders, obesity or cancer. WPI; 2004-365505/34. P-PSDB; ADN42982.

Murage J, Tang TY,

Nguyen DB, Ramkum Tran UK, Wang JT,

Zheng W;

Ison CH,

Claim SEQ D Ö 289pp; English.

The invention describes an isolated human secreted protein (SECP) copypeptide. Also described are: an isolated polynucleotide encoding the polypeptide; a recombinant polynucleotide; comprising a promoter sequence operably linked to the polynucleotide; a cell transformed with the recombinant polynucleotide; a transgenic organism comprising the recombinant polynucleotide; a method of producing the polypeptide; an isolated antibody that specifically binds to the polypeptide; a method of detecting a trarget polynucleotide in a sample; a method for treating a coverexpression of functional SECP; a method of screening a compound for compound that specifically binds to, or that modulates the activity of, the polypeptide; a method of screening a compound that specifically binds to, or that modulates the activity of, the polypeptide; a method of assessing toxicity of a test compound; a compound that specifically binds to, or that modulates the activity of, the polypeptide; a method of assessing toxicity of a test compound; a compositio test for a condition or disease associated with the expression of SECP in a biological sample; a method of diagnosting a condition or disease associated with the expression of SECP in a subject; a composition comprising the antibody and a carrier, or the polypeptide, or a sample; a method of purifically a method of detecting the polypeptide, or a sample; a method of proposition profile of a sample that contains affixed in distinct physical locations on a solid substrate, where at least one of the nucleotide molecules comprises a first oligonucleotide

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ESULT 10 AK52479 D AAK52479 standard; cDNA; 1966

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Human polynucleotide SEQ ID NO 2008

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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

Homo sapiens.

X N WO200157190-A2.

PD 09-AUG-2001.

F 05-FEB-2001; 2001WO-US004098.

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. 20-JUN-2000; 2000US-00598075. 19-JUL-2000; 2000US-00620325. 01-SEP-2000; 2000US-00654936. 15-SEP-2000; 2000US-00663561. 20-OCT-2000; 2000US-00693325. 30-NOV-2000; 2000US-00728422.

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1170; Conservative
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                         GGGCGATGGGTTGGGGGTGCCCACGGTGACAGCCACCAGGATCCTAAAGGGGCAGAAGAA
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/product= "Ecogpt"
/note= "E.coli xanthine-guanine
/ransferase gene"
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amma; fusion protein;
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bassay; E.coli;
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                      AACCCCGGGGCTTCTACCTCTTCGTGGAGGGAGGCCGCATTGACCACGGTCACCA
                                                   AACACGACACGTGGGAATGAGGTCACGTCTGTGATCAACCGGGCCAAGAAAGCAGG
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                                                                                                             GATGGGATGGGGGTGCCTACGGTGACAGCCACTCGGATCCTAAAGGGGCAGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1018.2; DB 2;
Pred. No. 1.8e-237;
0; Mismatches 253;
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1580

545

2000

845

725

665

1760

1700

1460

305

1400

245

1280

1220

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RESULT 14
AAT27393
ID AAT27393;
XX AAT27393;
AAT2739
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                            WPI; 1996-203155/21
P-PSDB; AAW03141.
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                                                                                                                                                                                                                               19-MAR-1996
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                                                                                                                                                                                  -SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH1-hinge-linker-alkaline
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
212. .503
/*tag= a
/note= "precise start position is unclear"
892. .2372
/*tag= b
/transl_except= pos:948. .950, aa:Ser
/transl_except= pos:951. .953, aa:Thr
/note= "end position corresponds to termination codon;
nucleotides 906. .956 encode a 17 amino acid linker and
nucleotides 957. .2366 are derived from the alkaline
phosphatase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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chimera; immun;
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Best Local Similarity
Matches 1160; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The gene coding for numangene coding for either the chain or an antibody light chain or one of which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant alkarııc
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                             TATGTGTGGAACCGCACTGAGCTCATGCAGGCGTCCCTGGACCAGTCTGTGACCC
                                                       TATGTGTGGAACCGCACTGCGCTCCTTCAGGCGGCCGATGACTCCAGTGTAACAC
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phosphatase (AP)-antibody fusion of antibody heavy or light chain, protein -useful as

40-43; 44pp; Japanese

The gene coding for human alkaline phosphatase is fused downstream of a gene coding for either the variable and CH1 regions of an antibody heavy chain or an antibody light chain. Coexpression of the H- and L-chain sequences, one of which is fused to the AP gene, results in production of AP-labelled antibodies suitable for use in immunoassays. The present sequence is an insert from plasmid pCHIP-1 coding for human IgG heavy chain constant region sequences (CH1-hinge) fused to a partial AP-coding region via a 17 amino acid linker

BP; 481 A; 781 0 710 G; 400 T; Ç, 0 Other;

Conservative 68.38; 0; Score 1008.8; DB 2; Pred. No. 3.1e-235; Mismatches 252; Indels Length Gaps 0

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Sequence 4, Appli Sequence 3, Appli	equence 16868,	equence 1586, A	equence 13264,	equence 22, App	equence 22, App	equence 22, App	equence 11859,	equence 1, Appl	equence 9, Appl	equence 9, Appl	equence 9, Appl	equence 17, App	equence 17, App	equence 5, Appl	equence 5, Appl	equence 3, Appl

## ALIGNMENT

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RESULT 1
US-09-305-681-1
; Sequence 1, Application
; Patent No. 6406899
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/305,681

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1798 base pairs

TYPE: nucleotide

STRANDEDNESS: single strand

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA
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Best Local Simil
Matches 1462; (
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RESULT 2
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APPLICANT:

TITLE OF INVENTION: Highly active alk

NUMBER OF SEQUENCES: 54

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/305,681

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2460 base pairs

TYPE: nucleotide

STRANDEDNESS: single strand

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

JS-09-305-681-3
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Best Local Simil
Matches 1388; (
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RESULT 3
US-09-305-681-5
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; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: H
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/305,681
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2542 base pairs
TYPE: nucleotide
STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
JS-09-305-681-5
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Best Local Similarity 93.9%;

Matches 1381; Conservative
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US-08-867-352-20
; Sequence 20, Application
; Patent No. 6060273
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               TITLE OF INVENTION: Multicistronic (
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/387,847
FILING DATE:
THEORY FOR IT WO
INFORMATION
SEQUENCE C
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AUTHORS: Mil
JOURNAL: J.
VOLUME: 261
PAGES: 3112-
DATE: 1986
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AUTHORS: I
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Query Match 67.9%;
Best Local Similarity 80.2%;
Matches 1177; Conservative
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NAME/KEY: CDS
LOCATION: 43..1560
OTHER INFORMATION: 1
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STRANDEDNESS: sin
TOPOLOGY: linear
OLECULE TYPE: cDNA
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; Sequence 12, Applicat:
; Patent No. 6632978
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GENERAL INFORMATION:
APPLICANT: Kaslin, Edgar
APPLICANT: Luyten, Marcel
APPLICANT: Zerwes, Hans-Gunter
TITLE OF INVENTION: Transgenic Animals For St
TITLE OF INVENTION: Regulation Of Genes
FILE REFERENCE: 4-31176A
CURRENT APPLICATION NUMBER: US/09/693,011
CURRENT FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 4989
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: DNA CONSTRUCT
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; OTHER INFORMAT:
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RESULT 6
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: Sequence 11, Application US/09693011
: Patent No. 6632978
: GENERAL INFORMATION:
: APPLICANT: Kaslin, Edgar
: APPLICANT: Luyten, Marcel
: APPLICANT: Zerwes, Hans-Gunter
: TITLE OF INVENTION: Transgenic Animals Follitle OF INVENTION: Regulation Of Genes
: FILE REFERENCE: 4-31176A
: CURRENT APPLICATION NUMBER: US/09/693,011
: CURRENT FILING DATE: 2000-10-20
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 5083
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: DNA CONSTRUCT
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tches 1176; Conservative 0; Mismatches 292  6 CCTCATCCCAGCTGAGGAGAAAACCCCGCCTTCTGGA	TYPE: DNA  TYPE: DNA  ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: synthetic expression plasmid S-09-932-581-25  Query Match Best Local Similarity  80.1%: Pred. No. 8.4e-24	ENT FILING R APPILING	GENERAL INFORMATION: APPLICANT: Andrews, William H. APPLICANT: Foster, Christopher APPLICANT: Fraser, Stephanie APPLICANT: Mohammadpour, Hamid TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: TELOMERASE FILE REFERENCE: SIER-005 CURRENT APPLICATION NUMBER: US/	1446 CACCGCCACCAGCATCCCCGACTAGGGT 1473  Y 1446 CACCGCCACCAGCATCCCCGACTAGGGT 1473  b 2574 CGGCACCACCGACGCCGCGCACCCGGGT 2601  ESULT 7 S-09-932-581-25 Sequence 25, Application US/09932581	2394 GCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCACGCAGGCGAGGACGTGGCGGTGTT 24  1326 CGCGCGAGGCCCGCAGGCGCACCCTGGTGCACGCGCGGAGGAGACCTTCGTGGCGCA 13	AAGGCCTTAGACAGCAAGTCCTACACCTCCATCCTCTATGGC	Qy 1026 GGCTAACGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAGACCACTCCCA 1085
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US-09-693-011-10
; Sequence 10, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaslin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zerwes, Hans-Gunter
TITLE OF INVENTION: Transgenic Animals For St
TITLE OF INVENTION: Regulation Of Genes
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kaslin, Edgar
APPLICANT: Luyten, Marcel
APPLICANT: Zerwes, Hans-Gunter
TITLE OF INVENTION: Transgenic Animals For St
TITLE OF INVENTION: Regulation Of Genes
FILE REFERENCE: 4-31176A
CURRENT APPLICATION NUMBER: US/09/693,011
CURRENT FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Artificial
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Sequence 20, Application US/09837863; Patent No. 6468754; GENERAL INFORMATION:
APPLICANT: Greene, Amy
APPLICANT: Zhou, Hua
APPLICANT: Thode, Silke
APPLICANT: Jarnigan, Kurt
TITLE OF INVENTION: Vector and Method fo
TITLE OF INVENTION: of an Integrated DN
FILE REFERENCE: 025.1US
CURRENT APPLICATION NUMBER: US/09/837,86
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; PRIOR APPLICATION NUMBER: US 60; PRIOR FILING DATE: 2000-04-18; NUMBER OF SEQ ID NOS: 27; SOFTWARE: PatentIn version 3.0; SEQ ID NO 20; LENGTH: 7076; TYPE: DNA; ORGANISM: vector US-09-837-863-20
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US-09-837-863-21
; Sequence 21, Applicat;
; Patent No. 6468754
; GENERAL INFORMATION:
                                                                                                                                                    ; LENGTH: 7076
; TYPE: DNA
; ORGANISM: vector
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APPLICANT: Zhou, Hua
APPLICANT: Thode, Silke
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                                                                      Score 1000.8; DB 4;
Pred. No. 9e-242;
0; Mismatches 292;
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Sequence 19, Application US/09837863;
Patent No. 6468754;
GENERAL INFORMATION:
APPLICANT: Greene, Amy
APPLICANT: Thode, Silke
APPLICANT: Thode, Silke
APPLICANT: Jarnigan, Kurt
TITLE OF INVENTION: Vector and Method for Targeted Replacement and
TITLE OF INVENTION: of an Integrated DNA Sequence
FILE REFERENCE: 025.1US
CURRENT APPLICATION NUMBER: US/09/837,863
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/198,498
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
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SEQ ID NO 1
LENGTH: 7
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Best Local Similarity 80.1%;
Matches 1176; Conservative
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                                                                                                                                                                                                                                                   TYPE: DNA
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Pred. No. 9e-242;
D; Mismatches 292; Indels
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APPLICANT: Thode, Silke
APPLICANT: Jarnigan, Kurt
TITLE OF INVENTION: Vector and Method for Tar
TITLE OF INVENTION: of an Integrated DNA Sec
FILE REFERENCE: 025.1US
CURRENT APPLICATION NUMBER: US/09/837,863
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: US 60/198,498
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 7092
TYPE: DNA
ORGANISM: vector
US-09-837-863-22
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RESULT 14
US-09-837-863-27
; Sequence 27, Application U
; Patent No. 6468754
; GENERAL INFORMATION:
APPLICANT: Greene, Amy
APPLICANT: Zhou, Hua
; APPLICANT: Thode, Silke
; APPLICANT: Jarnigan, Kur
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; TITLE OF INVENTION: of an Integrated DNA Se;
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 7573
; TYPE: DNA
; ORGANISM: vector
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RESULT 15
US-08-752-307B-1
; Sequence 1, Application
; Patent No. 5952171
; GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows Ve
SOFTWARE: FastSEQ for Windows Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,30
FILING DATE: 19-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McCarthy, Sean A.
APPLICANT: Gearing, David P.
APPLICANT: Levinson, Douglas A.
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING OF TITLE OF INVENTION: ENCODING NOVEL SECRETED NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-752-3078-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATIC
NAME: Meiklejohn, Ph PREGISTERMANICATION
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US-10-053-637-27
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## ALIGNMENTS

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RESULT 1
US-09-911-132A-1
; Sequence 1, Application US/099111;
; Publication No. US20030096341A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Expression of Alkaline Photo File Reference: RDID 0073US
; CURRENT APPLICATION NUMBER: US/09/911,132A
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 38
; COFTWARE: PatentIn version 3.1
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US-10-395-790A-1

Sequence 1, Application US/10395790A;

Publication No. US20040072316A1

GENERAL INFORMATION:

APPLICANT: Roche Diagnostics Corp.

TITLE OF INVENTION: Production of weakly active or institute of INVENTION: and their expression in yeast

TITLE OF INVENTION: and their expression in yeast

FILE REFERENCE: RDID 02028US

CURRENT APPLICATION NUMBER: US/10/395,790A

CURRENT FILING DATE: 2003-03-24

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 1

LENGTH: 1464

TYPE: DNA

ORGANISM: Bovine
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LOCATION: (1)...
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APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONE
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
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US-10-053-637-11

Sequence 11, Application US/10053637

Publication No. US20030158132A1

GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE

TITLE OF INVENTION: METHOD OF ENHANCI)
FILE REFERENCE: 206211

CURRENT APPLICATION NUMBER: US/10/053

CURRENT FILING DATE: 2002-01-22

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 1675

TYPE: DNA

COCANTEM. Artificial Sections
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 ORGANISM: Artificia FEATURE: OTHER INFORMATION: NAME/KEY: CDS
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Best Local Similarity 80.1%;

Matches 1178; Conservative
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OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (1544)..(1663)
OTHER INFORMATION: decorsin d
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RESULT 5
US-10-053-637-19
; Sequence 19, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCI
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
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OTHER INFORMATION: SEAP/MK fus
NAME/KEY: CDS
LOCATION: (11)..(1735)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1732)
OTHER INFORMATION: MK domain
S-10-053-637-19
                                            Query Ma
Best Loc
Matches
                                                                                                                                                                 TYPE: DNA ORGANISM:
                                            / Match 67.9%; Local Similarity 80.1%; 1es 1178; Conservative
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RESULT 6
US-10-053-637-15
; Sequence 15, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING I FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,63'
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
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OTHER INFORMATION: SEAP HINAME/KEY: CDS
LOCATION: (11)..(1765)
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NAME/KEY: misc_feature
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RESULT 7
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; Sequence 23, Applicati
; Publication No. US2003
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, I
; TITLE OF INVENTION: P
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LOCATION: (11)..(1903)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1900)
OTHER INFORMATION: VEGF121 c
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Matches 1178;
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CURRENT APPLICATION NUMBER: US/10/053,637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
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LOCATION: (1538)..(1591)
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CURRENT APPLICATION NUMBER: US/10/053,637
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                                                                                Sequence 5, Application US/10053637

; Publication No. US20030158132A1

; GENERAL INFORMATION:

; APPLICANT: KOVESDI, IMRE

; TITLE OF INVENTION: METHOD OF ENHANCING BONI

; FILE REFERENCE: 206211

; CURRENT APPLICATION NUMBER: US/10/053,637

; CURRENT FILING DATE: 2002-01-22

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1
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LENGTH: 19
TYPE: DNA
ORGANISM:
FEATURE:
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Best Local Similarity 80.2%;
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LOCATION: (11)..(15
OTHER INFORMATION:
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RESULT 10
US-09-908-943A-127
; Sequence 127, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
Alfredo G.
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APPLICANT: Yan, Riqiang
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Gurney, Mark E.
APPLICANT: Emmons, Thomas L.
APPLICANT: Bienkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BE'
FILE REFERENCE: 29915/00281A.US1
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 1728
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; Sequence 4, Application US/10071645
; Publication No. US20030148389A1
; GENERAL INFORMATION:
APPLICANT: Bihain, Bernard
; APPLICANT: Bour, Barbara
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Schizophrenia Related Ge;
FILE REFERENCE: 92.US2.CIP
; CURRENT APPLICATION NUMBER: US/10/071,645
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223,482
; PRIOR APPLICATION NUMBER: PCT/IB01/01891
; PRIOR FILING DATE: 2001-07-26
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WS-10-182-094-7

US-10-182-094-7

Sequence 7, Application US/10182094

Publication No. US20040019193A1

GENERAL INFORMATION:
APPLICANT: Liang, Peng

ITILE OF INVENTION: MOB-5/HMOB-5 AS A CANCER

CURRENT APPLICATION NUMBER: US/10/182,094

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: US 60/178,185

PRIOR FILING DATE: 2000-01-26

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7
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Best Local S
Matches 1176
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FEATURE:
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10-182-094-7
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Pred. No. 3.1e-285;
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; Sequence 9, Application US/10182094
; Publication No. US20040019193A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; TITLE OF INVENTION: MOB-5/HMOB-5 AS A CANCI
; FILE REFERENCE: 22000.0091U3
; CURRENT APPLICATION NUMBER: US/10/182,094
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: US 60/178,185
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NUMBER OF SEQ ID 1
SOFTWARE: FASTSEQ
SEQ ID NO 9
LENGTH: 2121
TYPE: DNA
ORGANISM: Artifi
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NOS: 22
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Pred. No. 3.1e-285;
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RESULT 14
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; Sequence 22, Ap
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APPLICANT: Moore, Margaret D.
APPLICANT: Chada, Sunil
TITLE OF INVENTION: NON-IMMUNOGEN
TITLE OF INVENTION: MARKERS FOR U
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 7
                                                                                                                                                                                                                                                                                                       GENERAL
                                  ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D
                                                                                                                                                             STREET:
CITY: !
STATE:
                                                                                                                                                COUNTRY:
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REFERENCE/DOCKET NUMBER: 9300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
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Best Local Simila
Matches 1176; Co
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LOCATION:
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Query Match Best Local Si Matches 1176;	TYPE: DNA  TYPE: DNA  ORGANISM: Artificial sequence FEATURE: OTHER INFORMATION: Description of artificial sequence: SEAP S-10-332-733-26	URRENT FILING DATE: 2003-06-10 UMBER OF SEQ ID NOS: 41 OFTWARE: PatentIn Ver. 2.1 Q ID NO 26	ENERAL INFORMATION: APPLICANT: Margarete Odenthal a TITLE OF INVENTION: Gene Expres TITLE OF INVENTION: In Myofibr FILE REFERENCE: 1472/68806 CURRENT APPLICATION NUMBER: US/	ESULT 15 S-10-332-733-26 Sequence 26, Application US/10332733 Publication No. US20040106565A1	QY 1446 CACCGCCACCAGCATCCCCGACTAGGG 1472 	1386 CATCATGGCCTTTGCGGGCTGGAGCCC	1326 CGCGCGAGGCCCGCAGGCGCACCTGGTGCACGGCGTGCAGGAGGAGACCTTCGTGGCGCACACCTTGGTGCACGCGCGCG	1266 GCAGCAGGCGTGCCCCTGGCTAGCGAGACCCACGGGGGGGG	1206 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCAAGCGAGGAACCCTCATACCG 12	1146 CAAGGCCTTAGACAGCAAGTCCTACACCTCCATCCTCTATGGCAATGGCCCAGGCTATGC 12	GICTICICITI	1026 GGCTAACGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAGACCACTCCCA 1	966 TGACGGCAAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGACAATGCCATCGCCAA 1	906 CAGGAACCCCGGGGCTTCTACCTCTTCGTGGAGGGAGGCCGCATTGACCACGGTCACCA 9	918 AGACTCCACACTGGACCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCCTGAGGG	
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Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called & 0.000925 using options -trim_alt "-trim_by cross match using options -minmatch plate: 35 row: H column: 01
Seq primer: CCCAGTCACGACGTTGTAAAACGHigh quality sequence stop: 733.
Location/Qualifiers
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A_BARC-East, Beltsville, MD 20705, USA
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/strain="Holstein"
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/clone="10BOV35_H01"
/dev_stage="Multiple"
/lab_host="DH108 T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector:
EcoRV; Site_2: NotI; Equimolar amounts
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Mammalia; Eutheria; Primates; Catarrhini; Ho.
1 (bases 1 to 1027)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Similarity 96.2%;
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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www.genoscope.cns.fr/cdna?s=CS0DE009DB05QP1&c=1699.f
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/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced Contact: Genoscope
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BX379970 Homo sapiens PLACENTA COT 25-NORMALIZED
clone CS0DI042YG09 5-PRIME, mRNA sequence.
BX379970
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (human)
                              Conservative
                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI042YG09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized
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                            Score 588.2; DE Pred. No. 1.2e-13; Mismatches 1
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BX458398 Homo sapiens PLACENTA 1
5-PRIME, mRNA sequence.
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BX458398.2 GI:47053565
Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 950)
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              Chordata;
Primates;
               Craniata; Vertebrata; Euteleostomi Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA clone CS0DE002YN2
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L Unpublished (2001)

On May 22, 2003 this sequence version replaced gi:31023009.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE002CG11QP1&c=1699.f
Location/Qualifiers
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Similarity 80.8%;
78; Conservative
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/db_xref="taxon:9606"
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Pred. No. 2.8e-131;
1; Mismatches 160;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster for more information about this allows.
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AL552555 Homo sapiens PLACENTA COT 25-NORMALIZED Homo clone CS0DI067YC24 5-PRIME, mRNA sequence.
AL552555
AL552555.3 GI:45857340
EST.
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                           For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO67BB12QP1&c=1699.f Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replace
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                                                                      CATCA
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  ccéccaagaagcrecadescacagacagcceccaagaaccrearcarcarcer
                       TAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTCTTCTT
                                                                    TCCCAGCTGAGGAGAAAACCCCGCCTTCTGGAACCGCCAGGCAGCCCAGGCCCT
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                                                                                                                                                                                                                              /clone="CSODIO67YC24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                         mol_type="mRNA"
db_xref="taxon:9606"
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Primates;
                                                                                                                                          Score 574.8; DB 1;
Pred. No. 2.3e-129;
l; Mismatches 168;
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Lunaryota, Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Primates; Catarrhini; Ho
E 1 (bases 1 to 1593)
S Clark, A.G., Glanowski, S., Nielson, R., Thomas
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J.
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution
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Homo sapiens (human)
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                                                                                                                                          sequence
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e, VIRTUAL
                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                            DNA
                   human-chimp-mouse
                                   Thomas, P., Kejariwal,
R., Lu, F., Murphy, B.,
Se, T.J., Sninsky, J.J.,
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partial sequence.
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hes 664; Conservative
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2 (bases 1 to 1593)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                                                                  ville, MD 20850, USA
sequence was made by sequencing genomic
based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        ACATACAACGTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCCTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 6e-126;
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EST.

Sus scrofa (pig)

M Sus scrofa (pig)

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; 1 (bases 1 to 772)

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., 1 Nonneman, D.J., Wray, J.E. and Keele, J.W.

Porcine EST collection using a normalized library collembryos representing early developmental stages Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
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/tissue_type="pooled"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1125)

S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30336211.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AI005ZB08QP1&c=1699.f.
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/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was
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Carninci, P., Shibata, Y., Hayatsu, N
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institu Physical and Chemical Research (RIKEN), Laboratory for Gen Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, CDNA library was preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in F Division of Experimental Animal Research in Riken contribuprepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
of 420. 563-573 (2002)
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6 (bases 1 to 2459)
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Functional annotation of a
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· &	Qy	Query Ma Best Loc Matches	ORIGIN			FEATURES				TITLE JOURNAL COMMENT	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM	H H	ហេស	Db Qy	Qy Db	D Q	g &	dd
66 TGATGTAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTCTTCTT 125 (	6 CCTCATCCCAGCTGAGGAGAAAACCCCGCCTTCTGGAACCGCCAGGCAGCCCAGGCCCT 65 	atch cal Similarity 81.0%; Pred. No. 2.4e-115; 626; Conservative 9; Mismatches 135; Indels 3; Gaps 3;	gested with Not I and cloned into the tes of the pCMVSPORT 6 vector. Library	one="CSODI076YD24" ssue_type="PLACENTA COT 25-NORMAI one_Tib="Homo sapiens PLACENTA CO te="1st strand cDNA was primed was primed was primed was prime was primed, dougle of the control	/organism="Homo   /mol_type="mRNA" /db xref="taxon:	נט:	o the Not I and EcoR V sites of the pCMVSPORT 6 vect normalized. Library was constructed by Life Technol ision of Invitrogen. This sequence belongs to sequence for the pcmvsport of the pcmvspor	ail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr t strand cDNA was primed with a NotI-oligo(dT) primer. F	act: Genoscope scope - Centre National de Sequencage 91 91006 EVRY cedex - France	Full-length cDNA libraries and normalizati Unpublished (2001) On Feb 15, 2001 this sequence version repl	Eukaryota; Metazoa; Chordata; Craniata; Ver Mammalia; Eutheria; Primates; Catarrhini; H 1 (bases 1 to 902) Li W.B. Gruber C. Jessee J. and Polaves D	AL553521.3 GI:45858290 EST. Homo sapiens (human) Homo sapiens	AL553521 AL553521 Homo sapi clone CS0DI076YD24 AL553521		1372 ACCTTCGTGGCGCACATCATGGCCTTTGCGGGCTGCGTGGAGCCCTACACCGAC 1425 	1313 ACGTGGCGGTGTTCGCGCGAGGCCCGCAGGCGCACCTG-GTGCACGGCGTGCAGGAGGAG 1371	1253 AACCCTCATACCGGCAGCAGGCGGCCGTGCCCCTGGCTAGCGAGACCCACGGGGGGGG	1193 GCCCAGGCTATGCGCTTGGCGGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGG 1252	
		COMMENT	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT 12 BX417625 LOCUS DEFINITION	מם אמ		γ	Db Qy	Qγ	Db Qy	Db Qy	Db Qy	D 29				Qy Db
Life Tech	ef@genoscope.cns.fr, Web : www.genoscope.cns.fr cDNA was primed with a NotI-oligo(dT) primer. Five r d, double-strand cDNA was digested with Not I and cl	10	to 936) uber,C., Jessee,J. and Polayes,D. cDNA libraries and normalization	EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Ch Mammalia; Eutheria; Pr	5-PRIME, mRNA sequence. BX417625 BX417625.2 GI:46955936	BX417625 RX417625 Homo ganieng	826 CGC-CARGGGTGCCCGGTATGTGTGGAA-CGCACTGAGCTCATGCAGGCTTCC 876	AMTAMAGCCAAGGTGGGACCARGCTGGACGGGAAGAATCTKGTGCAGGAATKGCTGGCG	665 ATGCCAGTGTGAATGGAGTCCGGAAGGACAAGCAGAACCTGGTGCAGGAATGGCAGGCCA 724	605 TGGGTGGAGGCCGAATGTACATGTTTCCTGAGGGGACCCCAGACCCTGAATACCCAGATG 664 	545 AGAATGGCTGCCAGGACATCGCCGCACAGCTGGTCTACAACATGGATATTGACGTGATCC 604	486 CGCGCACACGGTGAACCGAAACTGGTACTCAGACGCCGACCTGCCTG	GAAGGCCGTGGGAGTGGTGACCACCACCAGGGTGCAGCATGCCTCCCCAGCCGGGGCCTA	366 GTGCAACACGACACGTGGGAATGAGGTCACGTCTGTGATCAACCGGGCCAAGAAAGCAGG 425	306 GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTAAGTGCAGCCGCCCGC	CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCT 4			166 GGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCTTCCT 225 126 GGGGGATGGGATGGGGGTGCCTACGGTGACAGCCACTCGGATCCTAAAGGGGGCAGATGAA 185

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                                    TGCCAGTGTGAATGGAGTCCGGAAGGACCAAGCAGGTGCTGGTGCAGGAATGGCAGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 80.0%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE011YC17"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned intent the Not I and EcoRV sites of the pCMVSPORT_6 vector.
Library was not normalized."
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Pred. No. 3.8e-115;
Mismatches 152;
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ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt ', -trim_fasta. Vector identify
by cross_match using options -minmatch 12 -minscore 18

Plate: 6 row: J column: 03

Seq primer: CCTATTTAGGTGACACTATAGAAC

High quality sequence stop: 681.
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Mammalia; Eutheria;
Bovinae; Bos.
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                                                                                                                                                                                                                                /clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos
/mol_type="mRNA
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/strain="Holstein"
/db_xref="taxon:9913"
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Cetartiodactyla; Ruminantia; Pecora;
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Pred. No. 7.4e-114;
0; Mismatches 18;
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Mammalia, Eut
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AL540746
5-PRIME,
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AL540746.
EST.
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                                                                                                                                                                                                                           BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prinend enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, division of Invitrogen.
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Li,W.B., Gruber,C., Jessee,J. &
Full-length cDNA libraries and
Unpublished (2001)
On Feb 15, 2001 this sequence v
                                                                                                                                                                                This sequence belongs to sequence cluster 1699.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEOO4CAO3QP1&c=1699 Location/Qualifiers
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                                            /tissue_type="PLACENTA"
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/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                        /mol_type="mRNA"
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Mammalia; E
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replace Contact: Genoscope
                                                                                                   AL551653 Homo sapiens PLACENTA COT 25-NORMALIZED F
Clone CSODIO63YM05 5-PRIME, mRNA sequence.
AL551653
AL551653.3 GI:45856454
EST.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
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E (bases 1 to 1476)

S Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S.,
Eckstein,H., Kirschbaum,T. and Riebel,B.B.N.
Expression of alkaline phosphatase in yeast
Patent: JP 2002253269-A 4 10-SEP-2002;
F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2002253269-A/4
PD 10-SEP-2001
PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
PI RAINER MUELLER,JOHANN PETER THALHOFER,FRANK GEIPEL,WERNER PI HOELKE,
PI STEPHAN GLASER,HELLMUT ECKSTEIN,THOMAS KIRSCHBAUM, PI BETTINA BOMMARIUS NEE RIEBEL
PC C12N15/09,C12N1/19,C12N9/16//(C12N1/19,C12R1:645),(C12N1/19, PC C12R1:78),
PC C12N19/16,C12R1:645),(C12N9/16,C12R1:78),C12N15/00 CC Description of Artificial Sequence: Artificial FH Key
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  Score 1476; DB 6;
Pred. No. 1.3e-266;
Mismatches 0;
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Eckstein,H., Kirschbaum,T. and Bommarius,B.
Expression of alkaline phosphatase in yeast
Patent: EP 1176205-A 5 30-JAN-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE
Location/Qualifiers
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Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE Location/Qualifiers
GCATCAAGGTGCTCAATATGTTTGGAATAGAACTGCTTTGTTGCAAGCTGCTGAT
                                          GGGTGGTGGTAGAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCA
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/mol_type="unassigned DNA"
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AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T.  TITLE Production of inactive mutants or mutants with a low activity of an alkaline phosphatase and their expression in yeast  JOURNAL Patent: EP 1348760-A 9 01-OCT-2003;  Roche Diagnostics GmbH (DE); F.HOFFMANN-LA ROCHE AG (CH)  Location/Qualifiers  11476  /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Nucleic acid"	AX840892 LOCUS AX840892 LOCUS DEFINITION Sequence 9 from Patent EP1348760. ACCESSION AX840892 VERSION AX840892 VERSION AX840892.1 GI:39979035 KEYWORDS SOURCE Synthetic construct artificial sequences.  REFERENCE 1	Qy 1381 GCTCATATTATGGCTTTTTGCTGTTGTAACCATACACTGATTGTAATTTTGCCAGCT 1440	261 TACAGACAAGCTGCTGCTTCCATTGGCTAGTGAAACTCATGG	1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGGTCCAGGT 12	Qy 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACTTTGGTTACTGCTGATCAT 1080	Qy 901 TTGTCTAGAAATCCAAGAGGTTTTTACTTGTTTGAAGGTGGTAGAATTGATCATGGT 960	Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAATAGAACTGCTTTGTTGCAAGCTGAT 780  Oy 781 GATTCTAGTGTTACTCATTTGATGGGTTTTGAACCAGCTGATATGAAGTATAATGTT 840  Db 781 GATTCTAGTGTTACTCATTTGATGGGTTTTGTTTGAACCAGCTGATATGAAGTATAATGTT 840  OY 841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTT 900  B41 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTT 900  841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTT 900
Qy 841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTT 900	TIGITAATGGTGTTAGAAAGGATAAGCAAAATTTTGGTTCAAGAATGGCAA	FITGTCAAGATATTGCTGCTCAATTGGTTTACAATATGGATATTGATGTT 60	TIGIT GET GET TACTACTACTACTAGAGET TO AACATGCT TO TAGAGET 48	301 TACTTGTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTTTCTGCTGCTGCTAGATAC 36	QY  181 ATGAATGGTAAGTTGGGTCCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCT 240	Qy 61 GCTTTGGATGTTGCTAAGAAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTTG 120	ORIGIN  Query Match Best Local Similarity 99.9%; Pred. No. 5.3e-266; Matches 1474; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Qy 1 GAATTCTTGATTCCAGCTGAAGAAAAATCCAGCTTTTTGGAATAGACAAGCTGCTCAA 60

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Expression of alkaline phosphatase in yeast
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Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke, Eckstein,H., Kirschbaum,T. and Riebel,B.B.N. Expression of alkaline phosphatase in yeast Patent: JP 2002253269-A 1 10-SEP-2002; F HOFFMANN LA ROCHE AG
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Pred. No. 1.7e-148;
); Mismatches 394;
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RESULT 10
AX840884
LOCUS AX840884
DEFINITION Sequence
ACCESSION AX840884
VERSION AX840884
VERSION AX840884.

KEYWORDS Bos tauru
ORGANISM Bos tauru
Eukaryota
Mammalia;
REFERENCE 1
AUTHORS Mueller, F
TITLE Productic
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AX840884 1464 bp DNA linear PAT 16-DEC-2003 SION Sequence 1 from Patent EP1348760.

SION AX840884 1 GI:39979031 AX840884.1 GI:39979031

RDS .

Bos taurus (cow)

Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae Bovinae; Bos.

r,R., Thalhofer,J.P., Geipel,F., Hoelke,W. and Kirschbau tion of inactive mutants or mutants with a low activity on the phosphatase and their expression in yeast

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Similarity 73.2%;
70; Conservative
  CTTCTGTTAATGGTGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTAAGC
                                                      GTGGTGGTAGAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCAGATGATG
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NVQQDHTKDPTLAEMTEAALQVLSRNPRGFYLFVEGGRIDHGHHDGKAYMALTEAIMF
DNAIAKANELTSELDTLILVTADHSHVFSFGGYTLRGTSIFGLAPGKALDSKSYTSIL
YGNGPGYALGGGSRPDVNGSTSEEPSYRQQAAVPLASETHGGEDVAVFARGPQAHLVH
GVQEETFVAHIMAFAGCVEPYTDCNLPAPATATSIPD"
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/mol_type="unassigned
/db_xref="taxon:9913"
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1 (bases 1 to 1798)
Werner, H., Reina, M., Herumutto, B. and Johnshly active alkaline phosphatase
Patent: JP 1999332586-A 1 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
OS Bovidse
                                               Bos taurus
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovinae; Bos.
1 (bases 1 to 1798)
1 (bases 1 to 1798)
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Cetartiodactyla; Ruminantia; Pecora; Bovidae
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,W., Muller,R., Burtscher,H.
active alkaline phosphatase
: US 6406899-A 1 18-JUN-2002;
Location/Qualifiers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovinae; Bos.

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Burtscher, H.D., Mueller, R.D., Hoelke, W.D. and Millan, J.L.
High active alkaline phosphatase
Patent: EP 0955369-A 1 10-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
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/db_xref="taxon:9913"
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from Patent EP0955369.
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Bovinae; Bos.
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Patent: WO 03002736-A 26 09-JAN-2003;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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DHGHHDSKAYMALTEAVMFDNAIAKANELTSELDTLILVTADHSHVFSFGGYTLRGTS
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HGGEDVAVFARGPQAHLVHGVQEETFVAHVMAFAGCVEPYTDCNLPAPSGLSDAAHLA
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1385	TGCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAGAAGAAACTTTTGTTGCTCA	1326 1442
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605 721	GAATGGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGGATATTGATGTTATTTT	546 662
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22-APR-2004

(first entry)

standard; DNA; 1476 BP.

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## ALIGNMENTS

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ID ADI26515 s
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AC ADI26515;
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AC ADI26515;
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DT 22-APR-200
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OS Optimised
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OS Bos taurus
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FT CDS
PR 21-JUL-200
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P-PSDB; ADI26
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Kirschbaum T,
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HOFFMANN LA ROCHE & CO AG F
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           aryotic alkaline phosphatase, useful as diagnostic reagent sphorylation, by recombinant expression in yeast selected copy number.
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u T SEQ G ö ហ 23pp; German.

This invention describes a novel method of preparing eukaryotic alkaline phosphatase in yeast cells, comprising cloning an alkaline phosphatase gene sequence into different vectors, transforming, and expressing and purifying. A first vector is used containing a resistance gene against a selection marker and transformants that have integrated resistance gene and alkaline phosphatase gene into the genome are selected by growth on medium containing a low concentration of selection marker. The gene copy number is increased by multiple transformation and multiple transformants selected marker is introduced, its copy number increased as for the first resistance gene and clones selected that have many copies of the alkaline phosphatase gene and of both resistance genes, integrated into the genome. The vectors used in the method are phARP10-3 and pHAP10-3/9K. Preferred cells include methylotrophic yeast, particularly Pichia pastoris and Hansenula polymorpha and specifically P. pastoris X-33 transformed with pHAP10-3 yand pHAP10-3/9K. The amino acid sequence of bovine alkaline phosphatase is known and, working back from this, an optimised codon sequence was designed. This was assembled conventionally from 28 synthetic oligonucleotides to give a sequence having EcoRI and App718 recognition sites at the ends to facilitate cloning. The selection markers are particularly zeomycin and G418, respectively. The alkaline phosphatase with specific activity over 300, preferably 1000, units/mg and heat stability comparable with that for commercial enzymes. The expression system is resistant and stable and provides high-level expression without any selection pressure. This sequence represents an optimised bovine biapil polynucleotide.

Sequence 1476 B₽; 387 A; 223 ი, 346 <u>ი</u> 520 ij, O ď; 0 Other

Query Match Best Local Sin Matches 1476; 181 121 121 ტ ტ 61  $\vdash$ h 100.0%; Similarity 100.0%; 76; Conservative ( TTTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAATTTTGAAGGGTCAA rrrraggrangerarggrand 0 Score 1476; Pred. No. 0; Nismatches CAACTGTTACTGCTACTAGAATTTTGAAGGGTCAA CAATTCAAACTG DB ٠, و 0 Indels Length 1476; **;** Gaps 180 180 120 120 60 240 9

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RESULT 2
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AC ADE53386;
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DT 29-JAN-20 29-JAN-2004 stand (first entry) ard; DNA; 1476 BP.

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                                                                                                                                                                                                                This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with C ADE53385 and where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are C least 100-fold, relative to the wild type. The mutations described are C Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, C Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. C Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, i.e. they prevent non-specific binding of active alkaline phosphatase-C based conjugates to vessel walls or first antibodies, a phenomenon that may result in false positive results. The mutants have almost the same tertiary and quaternary structures as wild-type alkaline phosphatase, so tertiary appecific interference suppressors. This sequence represents a variant bovine alkaline phosphatase which includes an EcoRI site described in the disclosure of the invention.
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      TTTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAATTTTGAAGGGTCAA
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                                                                                                       phosphatase where the wild-type sequence is at least 77% homologous with 2C ADE53385 and where the alkaline phosphatase activity is reduced by at 2C least 100-fold, relative to the wild type. The mutations described are 3C Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, 3C Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for 3C Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, 3C i.e. they prevent non-specific binding of active alkaline phosphatase-3C based conjugates to vessel walls or first antibodies, a phenomenon that 3C may result in false positive results. The mutants have almost the same 3C certiary and quaternary structures as wild-type alkaline phosphatase, so 3C variant bovine alkaline phosphatase which contains an S92A mutation and 3C variant bovine alkaline phosphatase which contains an S92A mutation and 3C certiary and certiary and certiary and certiary and certiary and certiary structures as wild-type alkaline phosphatase.
                                                         Query Match
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Similarity 99.9%;
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This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with ADE53385 and where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based conjugates to vessel walls or first antibodies, a phenomenon that may result in false positive results. The mutants have almost the same tertiary and quaternary structures as wild-type alkaline phosphatase, so
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Claim æ •• SEQ. Z O 10; 35pp; German.

This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with C phosphatase where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are Rsp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, C Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. C Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, i.e. they prevent non-specific binding of active alkaline phosphatase-c based conjugates to vessel walls or first antibodies, a phenomenon that my result in false positive results. The mutants have almost the same tertiary and quaternary structures as wild-type alkaline phosphatase, so are very specific interference suppressors. This sequence encodes a variant bovine alkaline phosphatase which contains an H320N/G322F mutation and an EcoRI site described in the disclosure of the invention.

Sequence 1476 BP; 388 A; 222 C; 344 G; 522 T; 0 U; 0 Other;

Match

99.7**%**; 99.8**%**;

DB 10; Length 1476

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This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with C phosphatase where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are C Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, C Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for C Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. C Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, C i.e. they prevent non-specific binding of active alkaline phosphatase-C based conjugates to vessel walls or first antibodies, a phenomenon that C may result in false positive results. The mutants have almost the same C tertiary and quaternary structures as wild-type alkaline phosphatase, so are very specific interference suppressors. This sequence encodes a variant bovine alkaline phosphatase which contains an S92A/H320N/G322F mutation and an EcoRI site described in the disclosure of the invention.
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Query Match
99.6%; Score 1469.6; DB 10; Length 1476;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Score 845.6; DB 6; Pred. No. 8.6e-193; O; Mismatches 394;

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This invention describes a novel method of preparing eukaryotic alkaline phosphatase in yeast cells, comprising cloning an alkaline phosphatase (c) gene sequence into different vectors, transforming, and expressing and copurifying. A first vector is used containing a resistance gene against a selection marker and transformants that have integrated resistance gene and alkaline phosphatase gene into the genome are selected by growth on comedium containing a low concentration of selection marker. The gene copy number is increased by multiple transformation and multiple transformants selected on growth medium under high selection pressure. A second vector containing the alkaline phosphatase gene and a second resistance gene against a second marker is introduced, its copy number increased as for the first resistance gene and clones selected that have many copies of the alkaline phosphatase gene and of both resistance genes, integrated conton the genome. The vectors used in the method are phAplo-3 and phAplo-3/9K. Preferred cells include methylotrophic yeast, particularly Pichia pastoris and Hansenula polymorpha and specifically P. pastoris X-33 continued the phosphatase is known and, working back from this, an optimised codon sequence was designed. This was assembled conventionally from 28 synthetic oligonucleotides to give a sequence having EcoRI and CC hap718 recognition sites at the ends to facilitate cloning. The selection markers are particularly zeomycin and G418, respectively. The alkaline phosphatase with specific activity over 3000, preferably 10000, units/mg and heat stability comparable with that for commercial enzymes. The scyression without any selection pressure. This sequence represents the bovine biapii gene.
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Kirschbaum
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bovine; b
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This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with ADE53385 and where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for

Disclosure;

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P-PSDB;
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AC ADN4

The invention describes an isolated human secreted protein (SECP) polypeptide. Also described are: an isolated polynucleotide encoding the polypeptide; a recombinant polynucleotide; a cell transformed with the recombinant polynucleotide; a transgenic organism comprising the recombinant polynucleotide; a method of producing the polypeptide; an isolated antibody that specifically binds to the polypeptide; a method of detecting a transge polynucleotide; a method of screening a compound for condition associated with decreased expression or disease or condition associated with decreased expression or effectiveness as an agonist or antagonist of the polypeptide or in compound that specifically binds to, or that modulates the activity of, the polypeptide; a method of assessing toxicity of a test compound; a diagnostic test for a condition or disease associated with the expression of SECP in a biological sample; a method of diagnosing a condition or disease associated with the expression of SECP in a subject; a gonist or antagonist compound and an excipient a method of preparing a polypological sample; a method of diagnosing a condition or associated with the expression of SECP in a subject; a gonist or antagonist compound and an excipient a method of preparing a polypological sample; a method of diagnosing the polypeptide, or associated with the expression of secreting the polypeptide, or associated with a method of preparing a polypological sample; a method of diagnosing the polypeptide in a sample; a method of preparing a polypeptide; a method of preparing a polypeptide; a method of preparing a sample; a method of diagnosing the polypeptide of a sample that contains on a solid substrate, where at least one of the nucleotide molecules comprises a first oligonucleotide or polypucleotide sequence specifically hybridizable with at least 30 or polymucleotide sequence specifically hybridizable with at least 30
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CC contiguous nucleotides of the target polynucleotide. The polypeptide is CC useful for preparing a composition for diagnosing or treating a disease CC or condition associated with decreased expression or overexpression of CC functional SECP e.g. autoimmune disorders, obesity or cancer. This CC sequence encodes a human secreted protein.

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SQ Sequence 1702 BP; 339 A; 562 C; 513 G; 288 T; 0 U; 0 Other;

Query Match

41.6%; Score 613.8; DB 12; Length 1702;

Best Local Similarity 64.3%; Pred. No. 4e-137;
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Mismatches

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ACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAAGAATGGT ACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAAGGCTGGTAAGGCT AGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTTTTGTCTAGAAAT ATTTGATGGGTTTGTTTGAACCAGCTGATATGAAGTATAATGTTCAACAAGATCAT scaagracaterfricccargeegaccccaeacccreaetacccaecreatecaec GAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCAGATGATGCTTCT iggacatogocactoagotoatotocaacatogacattoacotoatocttogocoga GTGTTGTTACTACTACAGAGTTCAACATGCTTCTCCAGCTGGTGCTTACGCTCAT seccreaeaceccereecareeaccecrrcccaraccreecrcrercaaeaca GTCCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCTTTGTCTAAGACT AGAAGCTGCAGCCCATCCAGAAGGTCGCCAAGAACCTCATCCTCTTCCTGGGCGA CTGAAGAAGAAATCCAGCTTTTTGGAATAGACAAGCTGCTCAAGCTTTGGATGTT SAGGTTTTTACTTGTTTGTTGAAGGTGGTAGAATTGATCATGGTCATCATGATGGT regaccccrccrearegagargacagaggcreccrececcrecreagcagcaggaac ATCTCATGGGCCTCTTTGAGCCCGGAGACACGAAATATGAGATCCACCGAGACCCC CCTGGTÁTGTGGAÁCCGCÁCTGAGCTCATGCÁGGCGTCCCTGGÁCCAGTCTGTG CTCAATATGTTTGGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTCTAGTGTT aredant chec redace da ha conservada de la marca de ATGGTGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTAAGCATCAA TGAACCGCAACTGGTACTCAGATGCTGACATGCCTGCCTCAGCCCGGCCAGGAGGGG sadredreaccaccacacedrecaecacecciceccaeceecaecciacecacac reeses receches de la comparta del comparta del comparta de la comparta del la comparta de la comparta del la comparta del la comparta de la comparta del la compart AGAAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTTGTTTTTTGGGTGAT criga gea a gala con considera de la constanta 612 972 792 869 809 672 689 552 629 492 569 432 509 372 449 312 389 329 192 132 749 252 269 209

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and preventing encodes human a used in the example is located on a The present invention describes a method for detecting high-grade dysplasia (HGD) in cells of a mammalian tissue sample. Also described: (1) identifying an oesophageal tissue susceptible to oesophageal adenocarcinoma; (2) determining the predisposition of a mammalian tissue to a neo-plastic transformation by detecting HGD in cells of the tissue; and (3) detecting cancer in a patient. The method can be used in detecting HGD and cancer in cells of a mammalian tissue sample. The methods and compositions of the present invention can be used in treating and preventing HGD and cancer, and in gene therapy. The present sequence encodes human alkaline phosphatase intestinal precursor (PPBI), which is used in the exemplification of the present invention. The human PPBI gene chromosome

Seguence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;

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TITLE OF INVENTION: Highly active alkay NUMBER OF SEQUENCES: 54
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/305,681
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1798 base pairs
TYPE: nucleotide
STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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APPLICATION NUMBER: US/09
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2460 base pairs
TYPE: nucleotide
STRANDEDNESS: single stra
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
'S-09-305-681-3
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TITLE OF INVENTION: High
NUMBER OF SEQUENCES: 54
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, V

ICATION DATA:

NUMBER: US/09/305,681
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RESULT 3
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; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatib
OPERATING SYSTEM: PC-DOS/I
SOFTWARE: PatentIn Releas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2542 base pairs
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STRANDEDNESS: sin
TOPOLOGY: linear
MOLECULE TYPE: genou
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E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, V
ICATION DATA:
N NUMBER: US/09/305,681
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                                   AATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAAGGCTGG 425
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RESULT 4
US-08-867-352-20
; Sequence 20, Application
; Patent No. 6060273
; GENERAL INFORMATION:
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APPLICATION NUMBER: US/(FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/3 FILING DATE: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 25

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:

PDT TCATION NUMBER: US/08/867,352
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RESULT 5
US-09-263-933-1
; Sequence 1, Application US; Patent No. 6280940; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E; APPLICANT: Jackson, Rober; APPLICANT: Patick, Amy K.
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LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Int
FEATURE:
NAME/KEY: misc feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (MU
FEATURE:
NAME/KEY: misc feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/
FEATURE:
NAME/KEY: misc feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3
FEATURE:
NAME/KEY: misc
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OTHER INFORMATION
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ATION NUMBER: US/09/263,933
DATE: 1999-03-08
ATION NUMBER: 09/129,611
DATE: 1998-08-05
[D NOS: 33]
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ION: HCV NS4A
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ION: HCV NS3-NS4A cleavage site
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NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining
OTHER INFORMATION: plasmid
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OTHER INFORMATION:
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NAME/KEY: misc feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (
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LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP
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LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV N
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Pred. No. 1.2e-141;
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RESULT 6
US-09-263-933-8
; Sequence 8, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT;
FILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05

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NUMBER OF
SOFTWARE:
SEQ ID NO 8
                                                                                                                                                       LOCATION: (4375)...(4424)
OTHER INFORMATION: HCV NS.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4233)...(4394)
OTHER INFORMATION: HCV NS.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4395)...(4919)
OTHER INFORMATION: HCV NS.
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NAME/KEY: promoter
LOCATION: (794) . . (8
OTHER INFORMATION:
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OTHER INF
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OTHER INFORMATION: HCV E
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LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (
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LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 I
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/
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        : misc_feature
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US-09-263-933-15

; Sequence 15, Application US/09263933;
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEP FILE REFERENCE: 0125-0005A; CURRENT APPLICATION NUMBER: US/09/263,933; CURRENT FILING DATE: 1999-03-08; EARLIER APPLICATION NUMBER: 09/129,611; EARLIER FILING DATE: 1998-08-05; NUMBER OF SEQ ID NOS: 33
; COFTWARE: PatentIn Ver. 2.0
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FEATURE:
NAME/KEY: misc_f
LOCATION: (7915)
OTHER INFORMATIO
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NAME/KEY: misc f
LOCATION: (4395)
OTHER INFORMATIO
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(846)
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NAME/KEY: misc_feature
LOCATION: (1)..(774)
OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
OTHER INFORMATION: site
                                                                                    OTHER
                                                                                                                                 LOCATION: (4920).. (4991)
OTHER INFORMATION: HCV NS5A-NS5B cleavage site
                                                                                                                                                                                                                                                                                            NAME/KEY: misc
LOCATION: (4375
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
                                                                                                                                                                       FEATURE
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OTHER INFORMATI
                                                                                               LOCATION:
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                                                                                                                                                                                                                                 KEY: misc
ION: (4233)
INFORMATION
                                                                                   XEY: misc_feature
ION: (4992)..(6501)
INFORMATION: SEAP Protein
                                                                                                                                                                                                                                                                                                                               INFORMATION: HCV NS3-NS4A cleavage site
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(4920)
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(1019)
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(497)
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(1425)..(6500)
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                                    5)..(7945)
ION: MCS (1
                                                                                                                                                                                                                                   3) . . (4394)
ION: HCV NS
          nator
)..(8078)
                                                           feature
                                                                                                                                                                                   ON: HCV NS4B
                                                                                                                                                                                                                                                                                  ON: HCV NS4A-4B
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                                                                                                                                                           feature
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                                                                                                                                                                                                                                   NS4A
                                    (Multiple Cloning Site)
                                                                                                                                                                                    Domain
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Best Local Similarity 62.4%;

Matches 898; Conservative
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NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vacining
FEATURE:
NAME/KEY: misc feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining
OTHER INFORMATION: plasmid
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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atick, Amy K.
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CATION NUMBER: US/09/919,901
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LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2,
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NAME/KEY: misc_feat:
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NAME/KEY: misc_feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (
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LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP
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LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV N
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LOCATION: (4233)..(439)
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LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 I
OTHER INFORMATION: helicase
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LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for feature:
NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA
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APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE (
TITLE OF INVENTION: OF INHIBITORS
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
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                                                NAME/KEY: promoter LOCATION: (8080)..(8365)
OTHER INFORMATION: Vacinina virus promoter; early/late promoter
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ION: SEAP Protein
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ION: term T7
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ION: HCV NS5A-NS5B cleavage
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ION: HCV NS4B
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ION: HCV NS4A
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ION: HCV NS4A-4B clevage site
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ION: HCV NS3-NS4A cleavage site
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ION: HCV NS3 Domain.containing the serine protease and ION: helicase enzymes
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ION: T7 promoter
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Best Local Similarity 62.4%;
Matches 898; Conservative
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OTHER INFORMATION: plasmid
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APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

ITITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

ITITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

TOURS OF THE HEPATITIS C VIRUS PROTEASE
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NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining
OTHER INFORMATION: plasmid
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LOCATION: (2319)..(
OTHER INFORMATION:
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FEATURE:
NAME/KEY: misc_feat
LOCATION: (1)..(774
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LOCATION: (8560)..(11317)
OTHER INFORMATION: E. col
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LOCATION: (7938)..(8078)
OTHER INFORMATION: term
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LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (
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LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP
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LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV N
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NAME/KEY: misc_feature
LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV N
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LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV N
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LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV N
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LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Int
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LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV N
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LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E
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LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (
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APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CENTITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS CONTRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33
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SEQ ID NO 1
LENGTH: 13910
TYPE: DNA
ORGANISM: Artificial S
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APPLICANT: Jackson, Rol
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LOCATION: (1). (774)
OTHER INFORMATION: Vaco
OTHER INFORMATION: site
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NAME/KEY: misc_feat
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Best Local Similarity 62.4%;

Matches 898; Conservative
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LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
NAME/KEY: misc_feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple
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OTHER INFORMATION: MCS (MOTHER INFORMATION: MCS (MOTHER INFORMATION: MCV E2
OTHER INFORMATION: HCV E2
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NAME/KEY: misc fe
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OTHER INFORMATION: (
NAME/KEY: promoter
LOCATION: (8080)..()
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NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining
OTHER INFORMATION: plasmid
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LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domai
NAME/KEY: misc feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B
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LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage
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LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage
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RESULT 12
US-10-191-966-
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FEATURE:
OTHER INFORMATION: Description of Artific
NAME/KEY: CDS
LOCATION: (497)...(772)
NAME/KEY: CDS
LOCATION: (1425)...(6500)
NAME/KEY: CDS
LOCATION: (11877)...(10445)
NAME/KEY: CDS
LOCATION: (11877)...(10445)
NAME/KEY: CDS
LOCATION: (11877)...(12734)
NAME/KEY: CDS
LOCATION: (11877)...(12734)
NAME/KEY: misc feature
LOCATION: (11877)...(12734)
NAME/KEY: misc feature
LOCATION: (10191)...(10445)
NAME/KEY: misc feature
LOCATION: (194)...(816)
OTHER INFORMATION: T7 promoter
NAME/KEY: misc feature
LOCATION: (1426)...(1424)
OTHER INFORMATION: EMC/Internal Ribosome
NAME/KEY: misc feature
LOCATION: (1426)...(1437)
OTHER INFORMATION: MCS (Multiple Cloning
NAME/KEY: misc feature
LOCATION: (12319)...(4231)
OTHER INFORMATION: HCV MS3 Domain contain
NAME/KEY: misc feature
LOCATION: (2319)...(4231)
OTHER INFORMATION: HCV NS3 Domain contain
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SEQ ID NO 8
LENGTH: 1
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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33
NAME/KEY: misc f
LOCATION: (4233)
OTHER INFORMATIC
NAME/KEY: misc f
LOCATION: (4395)
OTHER INFORMATIC
NAME/KEY: misc f
LOCATION: (4920)
OTHER INFORMATIC
NAME/KEY: misc_f
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LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli
NAME/KEY: misc feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining
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OTHER INFORMATION: SEAP
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                                               TGCTTCTGTTAATGGTGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTAA
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEI

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05
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US-10-191-966-15
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GENERAL INFORMATION:
APPLICANT: Potts, Ka
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LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B clev
NAME/KEY: misc feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
NAME/KEY: misc feature
LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domain
NAME/KEY: misc feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B cl
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LOCATION: (1446)..(2318)
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LOCATION: (2319)..(4231)
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LOCATION: (7915)..(7945)
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LOCATION: (7938)..(8078)
OTHER INFORMATION: term TONAME/KEY: promoter
LOCATION: (8080)..(8365)
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LOCATION: (794)..(816)
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                                                                                                                  TGATGGTAAGGCTTATATGGCTTTGACTGAAGCTATTATGTTTGATAATGCTATTGCTAA 1025
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RESULT 14
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GENERAL INFORMATION:
APPLICANT: Kaslin, E
APPLICANT: Luyten,
APPLICANT: Zerwes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 897
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CURRENT APPLICATION NUMBER: US/09/693,011
CURRENT FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Luyten, Marcel
APPLICANT: Zerwes, Hans-Gunter
TITLE OF INVENTION: Transgenic Animals For TITLE OF INVENTION: Regulation Of Genes
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ORGANISM: Artificial
FEATURE:
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Pred. No. 2e-141;
Mismatches 543;
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CURRENT FILING DATE: 2000-
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APPLICANT: Zerwes, Hans-Gunter
TITLE OF INVENTION: Transgenic Animals For
TITLE OF INVENTION: Regulation Of Genes
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; Sequence 5, Application US/09911132A
; Publication No. US20030096341A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Expression of Alkaline Ph
; FILE REFERENCE: RDID 0073US
; CURRENT APPLICATION NUMBER: US/09/911,132A
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
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S-09-911-132A-5
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Best Local S
Matches 1476
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TYPE: DNA
ORGANISM: Artificial S
FEATURE:
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Pred. No. 0;
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US-10-395-790A-3

Sequence 3, Application US/10395790A

Publication No. US20040072316A1

GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corp.
TITLE OF INVENTION: Production of weakly active or institute of INVENTION: and their expression in yeast
FILE REFERENCE: RDID 02028US
CURRENT APPLICATION NUMBER: US/10/395,790A
CURRENT FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1476
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: codon-optimized alkaline phosphata
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RESULT 3
US-10-395-790A-8
; Sequence 8, Application US/10395790A
; Publication No. US20040072316A1

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GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corp.
TITLE OF INVENTION: Production of weakly active or TITLE OF INVENTION: and their expression in yeast FILE REFERENCE: RDID 02028US
CURRENT APPLICATION NUMBER: US/10/395,790A
CURRENT FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 1476
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: coding sequence for Ser92Ala muss-10-395-790A-8
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                           Score 1474.4;
Pred. No. 0;
0; Mismatches
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Query Match 99.8%; Score 1472.8; DB 16; Length 1476; Best Local Similarity 99.9%; Pred. No. 0; Matches 1474; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	ANIS TURI ER 1	SOFTWARE: PatentIn vers SEQ ID NO 9 LENGTH: 1476	FILE REFERENCE: RDID 02028US CURRENT APPLICATION NUMBER: US/10/395,790A CURRENT FILING DATE: 2003-03-24 NUMBER OF SEC ID NOS: 21	GENERAL INFORMATION: APPLICANT: Roche Diagnostics TITLE OF INVENTION: And thei	ESULT 4 S-10-395-790A-9 Sequence 9, Appli		1381 GCTCATATTATGGCTTTTGCTGGTTGTTGAACCATACACTGATTGTAATTTGCCAGCT 144	1321 GTTTTTGCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAGAAGAAACTTTTGTT 13	1261 TACAGACAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGGTGAAGATGTTGCT 13	1201 TATGCTTTGGGTGGTTCTAGACCAGATGTTAATGGTAGTACTAGTGAAGAACCATCT 126	1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGGTCCAGGT 120	1081 AGTCATGTTTTTCTTTTGGTGGTTACACTTTGAGAGGTACTTCTATTTTTGGTTTTGGCT 11	021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACTTTGATTT	961 CATCATGATGGTAAGGCTTATATGGCTTTGACTGAAGCTATTATGTTTGATAATGCTATT 1	901 TIGICIAGAAAICCAAGAGGIITIITACIIIGIIIGAAGGIIGIIAGAAIIGAICAIIGII 960 	841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTT 90	781 GATTCTAGTGTTACTCATTTGATGGGTTTGTTTGAACCAGCTGATATGAAGTATAATGTT 8
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Query Match  99.7%; Score 1471.2; DB 16; Length 1476;  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy  1 GAATTCTTGATTCCAGCTGAAGAAGATCCAGCTTTTTGGAATAGACAAGCTGCTCAA 60	WS-10-395-790A-10  Sequence 10, Application US/10395790A; Publication No. US20040072316A1  GENERAL INFORMATION: APPLICANT: Roche Diagnostics Corp. TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosp. TITLE OF INVENTION: and their expression in yeast FILE REFERENCE: RDID 02028US CURRENT APPLICATION NUMBER: US/10/395,790A CURRENT FILING DATE: 2003-03-24 NUMBER OF SEQ ID NOS: 21 SOFTWARE: PatentIn version 3.1 SEQ ID NO 10 LENGTH: 1476 TYPE: DNA ORGANISM: artificial sequence FEATURE: FOTHER INFORMATION: coding sequence for His320Asn/Gly322Phe mutant US-10-395-790A-10	Qy 1081 AGTCATGTTTTTCTTTTGGTGGTTACACTTTGAGAGGTACTTCTATTTTTGGTTTGGCT 1140
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US-10-395-790A-11

; Sequence 11, Application US/1039579; Publication No. US20040072316A1; GENERAL INFORMATION:

; APPLICANT: Roche Diagnostics Corp.

TITLE OF INVENTION: Production of 1

TITLE OF INVENTION: and their exp.

FILE REFERENCE: RDID 02028US; CURRENT APPLICATION NUMBER: US/10/:

; UMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1
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; Sequence 1, Application US/09911132A

; Publication No. US20030096341A1

; GENERAL INFORMATION:

; APPLICANT: Roche Diagnostics GmbH

; TITLE OF INVENTION: Expression of Al

; FILE REFERENCE: RDID 0073US

; CURRENT APPLICATION NUMBER: US/09/91

; CURRENT FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 38
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Publication No. US20040072316A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corp.
TITLE OF INVENTION: Production of weakly active or inactive mutants
TITLE OF INVENTION: and their expression in yeast
FILE REFERENCE: RDID 02028US
CURRENT APPLICATION NUMBER: US/10/395,790A
CURRENT FILING DATE: 2003-03-24
                                                                                            Query Match
Best Local Simila
Matches 1070; Co
                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1)...
OTHER INFORMATI
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ID NOS: 21
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Pred. No. 3.3e-180;
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US-10-053-637-9

; Sequence 9, Application US/10053637

; Publication No. US20030158132A1

; GENERAL INFORMATION:

; APPLICANT: KOVESDI, IMRE

; TITLE OF INVENTION: METHOD OF ENHANCING BONE DEI

; FILE REFERENCE: 206211

; CURRENT APPLICATION NUMBER: US/10/053,637

; CURRENT FILING DATE: 2002-01-22

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1597
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OTHER INFORMATION: SEAP/RGD fusion protein
NAME/KEY: CDS
LOCATION: (11)..(1585)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (1538)..(1570)
OTHER INFORMATION: RGD domain
US-10-053-637-9
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Best Local Similarity
Matches 898; Conser
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RESULT 10
US-09-006-298-22
; Sequence 22, Application U
; Patent No. US20020082224A1
; GENERAL INFORMATION:
APPLICANT: Jolly, Doug
APPLICANT: Moore, Marg
APPLICANT: Chada, Sun:
TITLE OF INVENTION: M
; NUMBER OF SEQUENCES:
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ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,298
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 898; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
-09-006-298-22
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pair:
TYPE: nucleic acid
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REGISTRATION NUMBER: 9300
REFERENCE/DOCKET NUMBER: 9300
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 622-4900
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ADDRESSEE:
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CITY: Seattle
STATE: Washing
COUNTRY: USA
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STRANDEDNESS: single
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E: SEED and BERRY LLP
6300 Columbia Center,
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RESULT 11
US-10-053-637-11
; Sequence 11, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
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Matches 898; Conservative
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Pred. No. 2.3e-120;
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RESULT 12
US-09-908-943A-127
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APPLICANT: Bienkowski, Mike J.
APPLICANT: Heinrikson, Robert L.
TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOI
FILE REFERENCE: 29915/00281A.US1
CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                            APPLICANT:
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RESULT 13
US-10-053-637-19
; Sequence 19, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; NUMBER OF SEQ ID NOS: 28
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LOCATION: (1538)..(1732)
OTHER INFORMATION: MK domain
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OTHER INFORMATION: SEAP
NAME/KEY: CDS
LOCATION: (11)..(1735)
OTHER INFORMATION:
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Sequence 15, Application US/10053637

Publication No. US20030158132A1

GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONI
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
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LOCATION: (11)..(1765)
OTHER INFORMATION:
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                                                NTGGCTTTTGCTGGTTGTGTTGAACCATACACTGATTGTAATTTGCCAGCTCCAGC
                                                                                                CAGTCAGCAGTGCCCCTGGACGAAGAGACCCACGCAGGCGAGGACGTGGCGGTGTT
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Sequence 23, Application US/10053637

publication No. US20030158132A1

GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONI
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEAP/VEGF12
NAME/KEY: CDS
LOCATION: (11)..(1903)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1900)
OTHER INFORMATION: VEGF121 dom
S-10-053-637-23
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GGGTGGTGGTAGAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCAGATGA
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Pred. No. 2.4e-120;
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1385	TGCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAGAAGAAACTTTTGTTGCTCA	1326	Ş
1380	gCAGCAGTCAGCAGTGCCCTGGACGAAGAGACCCACGCAGGCGAGGACGTGGCGGTGTT	1321	B
1325	ACAACAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGGTGGTGAAGATGTTGCTGTTTT	1266	ş
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1265	TTTGGGTGGTGGTTCTAGACCAGATGTTAATGGTAGTACTAGTGAAGAACCATCTTACAG	1206	Ş
1260	CAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTATACGGAAACGGTCCAGGCTATGT	1201	ర్జ
1205	TAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGGTCCAGGTTATGC	1146	Ş
1200		1141	망
1145	TGTTTTTTTTTTTGGTGGTTACACTTTGAGAGGGTACTTCTATTTTTGGTTTGGCTCCAGG	1086	Ş
1140		1081	g
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965	TAGAAATCCAAGAGGTTTTTACTTGTTTGTTGAAGGTGGTAGAATTGATCATGGTCATCA	906	Ş
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905	AGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTTTTGTC	846	Ş
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845	TAGTGTTACTCATTTGATGGGTTTGTTTGAACCAGCTGATATGAAGTATAATGTTCAACA	786	Ş
840		781	ర్థ
785	GCATCAAGGTGCTCAATATGTTTGGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC	726	Ş
780		721	뭥
725	TGCTTCTGTTAATGGTGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTAA	666	Ş
720	AGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCCTGAGTACCCCAGATGA	661	DЬ

Search completed: October 19, 2004, 23:49:31 Job time: 758.5 secs

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Result
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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

L Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIXEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Fround in Riken
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for f
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
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Encyclopedia Project of Genome Exploration Research Group in I
Genomic Sciences Center and Genome Science Laboratory in RIKE
Division of Experimental Animal Research in Riken contributed
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Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA Tel: 3015048416
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                                                                                                                                                                                                                                                                 /sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
ECORV; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
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was not normalized. Library was constructed by L division of Invitrogen.
This sequence belongs to sequence cluster 1699.f For more information about this cluster, see
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On May 22, 2003 this sequence version replaced
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Location/Qualifiers
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/db_xref="taxon:9606"

/clone="CSODE002YN21"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."
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Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Full-length cDNA libraries and
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e information about this cluster, see
www.genoscope.cns.fr/cdna?s=CSODE009DB05QP1&c=1699.f
Location/Qualifiers
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/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
/note="Vector: pCMVSPORT_6; 1st strand cDNA was digested with end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Mammalia; Eutheria; Primates; ....
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1 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Con May 8, 2003 this sequence version replaced (2001)
Con May 8, 2003 this sequence version replaced (2001)
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normalized. Library was constructed by Life Technologies, a
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ore information about this cluster, see //www.genoscope.cns.fr/cdna?s=CSODIO42ADO5QP1&c=1699.
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larity 63.3%;
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR 's
sites of the pCMVSPORT 6 vector. Library was normalized
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/db_xref="taxon:9606"
                                                                                                       type="mRNA"
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Pred. No. 1.8e-74;
; Mismatches 320;
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Best Local Similarity 35.6%;
Matches 512; Conservative
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Science 302 (5652), 1960-1963 (2003)
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2 (bases 1 to 1587)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sn
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exo
them based on alignment.
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genomic survey sequence.
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AY404255.1 GT.
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia; I
AGACATACAGTGTGGACAGACAGGTTCCAGACAGTGCAAGCACGGCCACCGCCTACCTG
                                                                                                                                             AGACTTACAATGTTGATAGACAAGTTCCAGATTCTGCTGGTACTGCTACTGCTTACTTGT
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/db_xref="taxon:10090"
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Re, T.J., Sninsky, J.J.,
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: Local Similarity
thes 556; Conserv
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AL552555.3
EST.
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lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f
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Genoscope - Centre National de So
BP 191 91006 EVRY cedex - France
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On Feb 15, 2001 this sequence version replace
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AL552555 Homo sapiens PLACENTA CO Clone CS0DI067YC24 5-PRIME, mRNA
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                             GTGTGGTGTTAAGGGTAATTACAGAACTATTGGTGTTTCTGCTGCTGCTAGATACAATCA
                                                                CAA
                                                                                                                             GGACAAACTGGGGCCTGAGTTACCCCCTGGCCATGGACCGCTTCCCATATGTGGCTCTGTC
                                                                                                                                                            TGGTAAGTTGGGTCCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCTTTGTC
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODI067YC24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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Office
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IMAGE: 7
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CF59156
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Email:
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                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Location/Qualifiers
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7023090 5', mRNA sequence.
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Cancer Genomics
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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GSS 15-DEC-2003

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Similarity 63.: 73; Conservative
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                     AGGGGGCTCAGTATGTGTGGAAATAAA
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                                                    CAAGGTGCTCAATATGTTTGGAATAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="whole body"
/clone Tib="NICHD_XGC_Swb1N"
/note="Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD_XGC_Swb1). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGAGTTCCAACAGTCACTGCCACCAGGATCTTAAGTGGGCAGATGAAGAGA
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Science 302
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal, Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse ortho
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Homo sapiens ALPPL2 gene,
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<u>ACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAAGAAAGCAGG</u>
                                                                                                                                                       CATACAGTGTAGACAAGCATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCT
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                     survey sequence.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="ALPPL2"
/locus_tag="HCM1829"
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1600 f
For more information about thi-
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Li,w.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)

On May 15, 2003 this sequence Contact: Genoscore
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e information about this cluster, see
www.genoscope.cns.fr/cdna?s=CSODEO11ABO9QP1&c=1699.f
Location/Qualifiers
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/clone="CSODE011YC17"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT): primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Matches 476; Conservative
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S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31275335.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f
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AL553521.3 GI:45858290
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Mammalia; Eutheria;
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                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI076YD24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR \
sites of the pCMVSPORT 6 vector. Library was normalized.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 2, 2003 this sequence version replaced
                                                                                                                                                                                          Homo
                                                                                                                                                                                                                      BX343739 I125 bp mRNA linear
BX343739 Homo sapiens PLACENTA COT 25-NORMALIZED F
clone CSODIO17YB14 5-PRIME, mRNA sequence.
BX343739
BX343739.2 GI:46270510
EST.
                                                  Contact
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI005ZB08QP1&c=1699.f. Location/Qualifiers
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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Institute of Physical and Chemical Research (RIKEN)
-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan: 81-45-503-9222
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les 453; Conservative
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RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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CAGATGATGCTTCTGTTAATGGTGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGC
                                                                     TTATTTTGGGTGGTGGTAGAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACC
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="E860129L22"
/cell_type="8 cells"
/dev_stage="8 cells embryo"
/clone_lib="RIKEN full-length enriched,
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Contact: bu-
USDA, ARS, US Me-
PO Box 166, Clay Center,
PO Box 166, Clay Center,
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called wire single pass sequencing. Bases called wire med with the aid of the trim_alt of column: 10

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Mammalia; E
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/clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_
/notary made with combined RNA from day-10, clay-15, day-25, and day-30 whole embryos."
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Eutheria;
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/lab_host="DH10B"
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mol_type="mRNA"

/db_xref="taxon:9823"
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                                                                                                       Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called ar
0.000925 using options -trim_alt '' -tr
by cross_match using options -minmatch
plate: 6 row: J column: 03
Seq primer: CCTATTTAGGTGACACTATAGAAC
High quality sequence stop: 681.
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Contact: Richard G. Baumann
Bovine Functional Genomics
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Baumann, R.G., Baldw
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/mol_type="mRNA"
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/db_xref="taxon:9913"
/clone="8BOV_6J03"
/sex="Female"
                                                                                            ity sequence stop: 681 Location/Qualifiers
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Eutheria;
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/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
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Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,Weckstein,H., Kirschbaum,T. and Riebel,B.B.N.
Expression of alkaline phosphatase in yeast Patent: JP 2002253269-A 1 10-SEP-2002;
F HOFFMANN LA ROCHE AG
OS Bos sp. (bovine)
PN JP 2002253269-A/1
PD 10-SEP-2002
PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
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L2N15/09, C12N1/19, C12N9/16//(C12N1/19, C12R1:645), (C12N1/19,

L2R1:78),

C12N9/16, C12R1:645), (C12N9/16, C12R1:78), C12N15/00 CC

Sion of alkaline phosphatase in yeast

Location/Qualifiers

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Location/Qualifiers
                                          /organism="Bos sp."
/mol_type="genomic DNA"
/db_xref="taxon:29061"
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Eutheria;
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             CAGCAAGACCACCAAGGACCCGACCCTGGCGAGATGACGGAGGCGGCCCTGCAAGTG
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Eukaryota; Metazoa; Chordata,
Mammalia; Eutheria; Cetartiodactyla; Number Servinae; Bos.

Bovinae; Bos.

Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Gleckstein,H., Kirschbaum,T. and Bommarius,B.
Expression of alkaline phosphatase in yeast
Patent: EP 1176205-A 1 30-JAN-2002;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE
Location/Qualifiers

1 .1476
"Bos taurus"

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                                                                                                                       TACCGGCAGCAGGCGGCCGTGCCCTGGCTAGCGAGACCCCACGGGGGCGAAGACGTGGCG
                TATGCGCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGGAACCCTCA
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Mammalia; E
Bovinae; Bo
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Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG Location/Qualifiers
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Eutheria;
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/db_xref="taxon:9913"
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/protein_id="CAE85444.1"
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JP 199332586-A/1.

Bos taurus (cow)

Ebytota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 1798)

New The Third of the phosphatase

Patent: JP 199332586-A 1 07-DEC-1999;

ROCHE DIAGNOSTICS GMBH

OS Bovidae

PN JP 199332586-A/1

PD 07-DEC-1999

PF 06-MAY-1998 DE 19819962:7

PR 05-MAY-1998 DE 19819992:7

PR 05-MAY-1998 DE 198199932:7

PR 05-MAY-1998 DE 19819992:7

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/mol_type="genomic DNA"
/db_xref="taxon:9913"
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Burtscher, H.D., Mueller, R.D., Hoelk
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Pred. No. 4e-267;
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Bovine alkaline phosphata Unpublished
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Manes, T., Hoylaerts, M.F., Millan, J.L.
Direct Submission
Submitted (05-MAR-1998) N
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Mammalia; Eutheria; (
Bovinae; Bos.
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                                                                    Werner, H., Reina, M., Herumutto, B. and Jo. Highly active alkaline phosphatase patent: JP 199332586-A 2 07-DEC-1999; ROCHE DIAGNOSTICS GMBH

OS Bovidae
PN JP 199332586-A/2
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOERUKU, REINA MULLER, HERUMUTLOUIS MILAN
PC C12N15/09, C12N1/15, C12N1/19, C12N1/2
C12N15/00, C12N5/00
CC
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Location/Qualifiers
FT Bource
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urce 1. .2460
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9913"
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90.7%;
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No. 1.1e-2
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RESULT 10
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Sequence 3
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1 (bases 1 to 2460)

1 (bases 1 to 2460)

Hoelke, W., Muller, R., Burtscher, H., Hoelke, W., Muller, R., Burtscher, H., Hoelke, W., Muller, R., Burtscher, H., Allers

Hoelke, W., Muller, R., Burtscher, H., Aller, Burtscher, Aller, Burtscher, Burtscher, Aller, Burtscher, Hoelke, Burtscher, Burtscher, Hoelke, Burtscher, Hoelke, Burtscher, Hoelke, Burtscher, Hoelke, Burtscher, H., Aller, Burtscher, Burtscher, H., Aller, Burtscher, H., Aller, Burtscher, H., Aller, Burtscher, H., Aller, Burtscher, Burtscher, H., Aller, Burtscher, Burtscher, H., Aller, Burtscher, Burt
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TGGCCTCTCCGACGCCGCGCACCTGGCGGCC
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/organism="unknown"
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SVGVVTTSRVQHASPAGAYAHTVNRNWYSDADLPADAQTYGCQDIATQLVNNMDIDVI
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IFGLAPSKASDNKSYTSILYGNGPGYVLGGGLRPDVNDSISEDPSYRQQAAVPLSSES
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/mol_type="mRNA"
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OS Bovidae
PN JP 1999332586-A/3
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOERUKU, REINA MULLER, HERUMUT LOUIS MILAN
PC C12N15/09, C12N1/15, C12N1/19, C12N1/2 C12N15/00, C12N5/00
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/organism="Bos taurus"
/mol_type="genomic DNA"
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Hoelke, W., Muller, R., Burtscher, H. and Highly active alkaline phosphatase Patent: US 6406899-A 5 18-JUN-2002;

Location/Qualifiers

1. .2542

/organism="unknown"
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Location/Qualifiers
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tive
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